<u>Amendments to the Claims</u>:

1.   (Previously Presented) A method for identifying a compound which inhibits or reduces pathogenicity of the same pathogen in at least two different eukaryotic organisms, said pathogen utilizing a common virulence factor to infect said eukaryotic organisms, said method comprising the steps of:

(a)   exposing said at least two different eukaryotic organisms, at least one of said organisms being a non-rodent, to said same pathogen in the presence of at least one candidate compound; and

(b)   detecting inhibition or reduction of pathogenicity of said same pathogen as an indication that said candidate compound inhibits or reduces pathogenicity of said same pathogen in each of said eukaryotic organisms as a consequence of affecting the function of said common virulence factor in said pathogen.

2.   (Original) The method of claim 1, wherein said pathogen is a bacterium.

3.   (Original) The method of claim 2, wherein said bacterium is *Pseudomonas aeruginosa*.

4.   (Original) The method of claim 2, wherein said bacterium is *Pseudomonas aeruginosa* UCBPP-PA14.

5.	(Original) The method of claim 1, wherein said eukaryotic organisms includes a vertebrate and a plant.

6.	(Original) The method of claim 1, wherein said eukaryotic organism includes a vertebrate and an invertebrate.

7.	(Original) The method of claim 1, wherein said eukaryotic organism includes a plant and an invertebrate.

8.	(Original) The method of claim 5 or claim 6, wherein said vertebrate is a mammal.

9.	(Original) The method of claim 6 or claim 7, wherein said invertebrate is a nematode.

10.	(Original) The method of claim 9, wherein said nematode is a member of the genus *Caenorhabditis*.

11.	(Original) The method of claim 5 or claim 7, wherein said plant is a member of the genus *Arabidopsis*.

12.   (Original) The method of claim 1, wherein each of said eukaryotic organisms is a plant.

13.   (Original) The method of claim 1, wherein each of said eukaryotic organisms is a vertebrate.

14.   (Original) The method of claim 1, wherein each of said eukaryotic organisms is an invertebrate.

15.   (Original) The method of claim 14, wherein said invertebrate is an insect.

16.   (Original) The method of claim 15, wherein said insect is a lepidopteran.

17.   (Original) The method of claim 16, wherein said lepidopteran is *Galleria* or *Plutella*.

18.   (Previously Presented) The method of claim 15, wherein said insect is a dipteran.

19.   (Previously Presented) The method of claim 18, wherein said dipteran is *Drosophila*.

20.   (Original) The method of claim 1, wherein said method utilizes the nematode fast killing assay.

21.   (Original) The method of claim 20, wherein said nematode fast killing assay involves the use of a *C. elegans* having a P-glycoprotein mutation.

22.   (Previously Presented) A method for identifying a compound which inhibits or reduces pathogenicity of the same pathogen in a nematode and a plant, said same pathogen utilizing a common virulence factor to infect said nematode and said plant, comprising the steps of:

(a) exposing said nematode and said plant to said same pathogen in the presence of at least one candidate compound; and

(b) identifying a compound that inhibits or reduces pathogenicity of said same pathogen in said nematode and said plant as a consequence of affecting the function of said common virulence factor in said same pathogen.

23.   (Original) The method of claim 22, wherein said pathogen is a bacterium.

24.   (Original) The method of claim 23, wherein said bacterium is *Pseudomonas aeruginosa* UCBPP-PA14.

25.   (Canceled).

26.   (Previously Presented) The method of claim 22, wherein said nematode is *Caenorhabditis elegans*.

27.   (Canceled).

28.   (Previously Presented) The method of claim 22, wherein said plant is *Arabidopsis*.

29.   (Original) The method of claim 22, wherein said method utilizes the nematode fast killing assay.

30.   (Original) The method of claim 29, wherein said nematode fast killing assay involves the use of a *C. elegans* having a P-glycoprotein mutation.

31.-45. (Canceled).